

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings in the application.

1-16. (Cancelled)

17. (Currently amended) A method of simultaneously detecting or quantifying a plurality ~~n~~ kinds of different target nucleic acids (Fa, Sa) each having a predetermined first partial sequence Fa and a predetermined second partial sequence Sa, wherein Fa is any one of partial sequences F1 to Fn, wherein n is an integer of 2 or more: are [F1, F2, ... Fn]; Sa is any one of partial sequences S1 to Sn, wherein n is an integer of 2 or more: are [S1, S2, ... Sn]; and (Fa, Sa) are (F1, S1), (F2, S2), ... (Fn, Sn), wherein n is an integer of 2 or more: [(F1, S1), (F2, S2), ... (Fn, Sn)], in a specimen comprising:

(a) preparing probes Aa, wherein Aa is any one of the probe groups A1 to An and wherein n is an integer of 2 or more: are [A1, A2, ... An] and Ba are [B1, B2, ... Bn] is any one of the probe groups B1 to Bn and wherein n is an integer of 2 or more,

said probes Aa being respective first probes each of which has a sequence F'a complementary to the respective first partial sequence Fa of the target nucleic acid (Fa, Sa) and a first binding molecule bound to the sequence F'a, wherein F'a is any one of the sequences F'1 to F'n and wherein n is an integer of 2 or more: are [F'1, F'2, ... F'n], and

said probes Ba being respective second probes each of which has a sequence S'a complementary to the respective second partial sequence Sa of the target nucleic acid and a flag bound to the sequence S'a, wherein said flag comprises four units SD, D0_j, D1_k, and ED, each having a desired sequence, and linked in the form of SD+ D0_j+ D1_k+ ED; wherein the flag sequences D0_j and D1_k are located between SD and ED and a combination of the D0_j and D1_k (D0_j, D1_k) being assigned respectively to the target nucleic acids (Fa, Sa); and wherein SD and ED are each primer sequences, wherein S'a are [S'1, S'2, ... S'n] is any one of the sequences S'1 to S'n and wherein n is an integer of 2 or more, and wherein j and k are arbitrary natural numbers,

(b) mixing the probes Aa and the probes Ba with specimens containing target nucleic acids (Fa, Sa) respectively, thereby hybridizing the first probes Aa with the respective

first partial sequences Fa of the target nucleic acids and simultaneously hybridizing the second probes Ba with the respective second partial sequence Sa of the target nucleic acids;

(c) ligating the first probes Aa and the second probes Ba, both being hybridized with the target nucleic acids (Fa, Sa), thereby obtaining probes (Aa+Ba);

(d) binding the first binding molecules of probe Aa to substances capable of being paired up therewith, thereby recovering the probes (Aa+Ba);

(e) dissociating the flag sequences (D0_j, D1_k);

(f) amplifying the flag sequences (D0_j, D1_k) by PCR, wherein the PCR uses a primer to which a marker substance is bound, and thereby obtaining the flag sequences (D0_j, D1_k) to which the marker substance is bound; and

(g) detecting or quantifying the marker substance of the flag sequences (D0_j, D1_k), thereby detecting or quantifying the target nucleic acids (Fa, Sa).

18. (Cancelled)

19. (Currently amended) The method according to claim 17, wherein step (e) further comprises:

amplifying the dissociated flag sequences (D0_j, D1_k) by PCR,

wherein the PCR uses a primer to which a second binding molecule is bound, and thereby obtains the flag sequences (D0_j, D1_k) to which the second binding molecule is bound[[:]], and

binding the second binding molecules of the flag sequences (D0_j, D1_k) to substances capable of being paired up therewith, thereby recovering the flag sequences (D0_j, D1_k).

20-21. (Cancelled)

22. (Previously presented) The method according to claim 17, wherein, in said step (d), said substance capable of being paired up with the first binding molecules are immobilized on beads such that the probes (Aa, Ba) are recovered by binding the probe (Aa, Ba) to the beads via the first binding molecules.

23. (Previously presented) The method according to claim 17, wherein said marker substance is a fluorescent substance such that the target nucleic acids are detected or quantified by quantifying the fluorescent substance.

24. (Cancelled)

25. (Previously presented) The method according to claim 17, wherein said flag sequences (D0_j, D1_k) are double stranded sequences.

26-33. (Cancelled)